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RAW SEQUENCE LISTING

DATE: 03/28/2002

PATENT APPLICATION: US/09/769,787

TIME: 12:59:18

Input Set : D:\P21129WO sequence listing.txt

Output Set: N:\CRF3\03282002\I769787.raw

P.S

C-11 <140> CURRENT APPLICATION NUMBER: US/09/769,787
 C-12 <141> CURRENT FILING DATE: 2001-01-26

3 <110> APPLICANT: Microbial Technics Limited
 4 Gilbert, Christophe FG
 5 Hansbro, Philip M
 7 <120> TITLE OF INVENTION: Proteins
 9 <130> FILE REFERENCE: PWC/P21129WO
 11 <140> CURRENT APPLICATION NUMBER: US/09/769,787
 12 <141> CURRENT FILING DATE: 2001-01-26
 14 <150> PRIOR APPLICATION NUMBER: GB 9816337.1
 15 <151> PRIOR FILING DATE: 1998-03-27
 17 <150> PRIOR APPLICATION NUMBER: US 60/125164
 18 <151> PRIOR FILING DATE: 1999-03-19
 20 <160> NUMBER OF SEQ ID NOS: 388
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 207
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Streptococcus pneumoniae
 29 <400> SEQUENCE: 1

ENTERED

30 Met Glu Glu Leu Val Thr Leu Asp Cys Leu Phe Ile Asp Arg Thr Lys
 31 1 5 10 15
 33 Ile Glu Ala Asn Ala Asn Lys Tyr Ser Phe Val Trp Lys Lys Thr Thr
 34 20 25 30
 36 Glu Lys Phe Ser Ala Lys Leu Gln Glu Gln Ile Gln Val Tyr Phe Gln
 37 35 40 45
 39 Glu Glu Ile Thr Pro Leu Leu Ile Lys Tyr Ala Met Phe Asp Lys Lys
 40 50 55 60
 42 Gln Lys Arg Gly Tyr Lys Glu Ser Ala Lys Asn Leu Ala Asn Trp His
 43 65 70 75 80
 45 Tyr Asn Asp Lys Glu Asp Ser Tyr Thr His Pro Asp Gly Trp Tyr Tyr
 46 85 90 95
 48 Arg Phe His His Thr Lys Tyr Gln Lys Thr Gln Thr Asp Phe Gln Gln
 49 100 105 110
 51 Glu Ile Lys Val Tyr Tyr Ala Asp Glu Pro Glu Ser Ala Pro Gln Lys
 52 115 120 125
 54 Gly Leu Tyr Met Asn Glu Arg Tyr Gln Asn Leu Lys Ala Lys Glu Cys
 55 130 135 140
 57 Gln Ala Leu Leu Ser Pro Gln Gly Arg Gln Ile Phe Ala Gln Arg Lys
 58 145 150 155 160
 60 Ile Asp Val Glu Pro Val Phe Gly Gln Ile Lys Ala Ser Leu Gly Tyr
 61 165 170 175
 63 Lys Arg Cys Asn Leu Arg Gly Lys Arg Gln Val Arg Ile Asp Met Gly
 64 180 185 190
 66 Leu Val Leu Met Ala Asn Asn Leu Leu Lys Tyr Ser Lys Met Lys

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67          195          200          205
71 <210> SEQ ID NO: 2
72 <211> LENGTH: 2233
73 <212> TYPE: PRT
74 <213> ORGANISM: Streptococcus pneumoniae
76 <400> SEQUENCE: 2
77 Met Gly Lys Gly His Trp Asn Arg Lys Arg Val Tyr Ser Ile Arg Lys
78   1          5          10          15
80 Phe Ala Val Gly Ala Cys Ser Val Met Ile Gly Thr Cys Ala Val Leu
81          20          25          30
83 Leu Gly Gly Asn Ile Ala Gly Glu Ser Val Val Tyr Ala Asp Glu Thr
84          35          40          45
86 Leu Ile Thr His Thr Ala Glu Lys Pro Lys Glu Glu Lys Met Ile Val
87          50          55          60
89 Glu Glu Lys Ala Asp Lys Ala Leu Glu Thr Lys Asn Ile Val Glu Arg
90   65          70          75          80
92 Thr Glu Gln Ser Glu Pro Ser Ser Thr Glu Ala Ile Ala Ser Glu Lys
93          85          90          95
95 Lys Glu Asp Glu Ala Val Thr Pro Lys Glu Glu Lys Val Ser Ala Lys
96          100          105          110
98 Pro Glu Glu Lys Ala Pro Arg Ile Glu Ser Gln Ala Ser Asn Gln Glu
99          115          120          125
101 Lys Pro Leu Lys Glu Asp Ala Lys Ala Val Thr Asn Glu Glu Val Asn
102          130          135          140
104 Gln Met Ile Glu Asp Arg Lys Val Asp Phe Asn Gln Asn Trp Tyr Phe
105   145          150          155          160
107 Lys Leu Asn Ala Asn Ser Lys Glu Ala Ile Lys Pro Asp Ala Asp Val
108          165          170          175
110 Ser Thr Trp Lys Lys Leu Asp Leu Pro Tyr Asp Trp Ser Ile Phe Asn
111          180          185          190
113 Asp Phe Asp His Glu Ser Pro Ala Gln Asn Glu Gly Gly Gln Leu Asn
114          195          200          205
116 Gly Gly Glu Ala Trp Tyr Arg Lys Thr Phe Lys Leu Asp Glu Lys Asp
117          210          215          220
119 Leu Lys Lys Asn Val Arg Leu Thr Phe Asp Gly Val Tyr Met Asp Ser
120   225          230          235          240
122 Gln Val Tyr Val Asn Gly Gln Leu Val Gly His Tyr Pro Asn Gly Tyr
123          245          250          255
125 Asn Gln Phe Ser Tyr Asp Ile Thr Lys Tyr Leu Gln Lys Asp Gly Arg
126          260          265          270
128 Glu Asn Val Ile Ala Val His Ala Val Asn Lys Gln Pro Ser Ser Arg
129          275          280          285
131 Trp Tyr Ser Gly Ser Gly Ile Tyr Arg Asp Val Thr Leu Gln Val Thr
132          290          295          300
134 Asp Lys Val His Val Glu Lys Asn Gly Thr Thr Ile Leu Thr Pro Lys
135   305          310          315          320
137 Leu Glu Glu Gln Gln His Gly Lys Val Glu Thr His Val Thr Ser Lys
138          325          330          335
140 Ile Val Asn Thr Asp Asp Lys Asp His Glu Leu Val Ala Glu Tyr Gln

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141	340	345	350
143	Ile Val Glu Arg Gly Gly His Ala Val Thr Gly Leu Val Arg Thr Ala		
144	355	360	365
146	Ser Arg Thr Leu Lys Ala His Glu Ser Thr Ser Leu Asp Ala Ile Leu		
147	370	375	380
149	Glu Val Glu Arg Pro Lys Leu Trp Thr Val Leu Asn Asp Lys Pro Ala		
150	385	390	395
152	Leu Tyr Glu Leu Ile Thr Arg Val Tyr Arg Asp Gly Gln Leu Val Asp		
153	405	410	415
155	Ala Lys Lys Asp Leu Phe Gly Tyr Arg Tyr Tyr His Trp Thr Pro Asn		
156	420	425	430
158	Glu Gly Phe Ser Leu Asn Gly Glu Arg Ile Lys Phe His Gly Val Ser		
159	435	440	445
161	Leu His His Asp His Gly Ala Leu Gly Ala Glu Glu Asn Tyr Lys Ala		
162	450	455	460
164	Glu Tyr Arg Arg Leu Lys Gln Met Lys Glu Met Gly Val Asn Ser Ile		
165	465	470	475
167	Arg Thr Thr His Asn Pro Ala Ser Glu Gln Thr Leu Gln Ile Ala Ala		
168	485	490	495
170	Glu Leu Gly Leu Leu Val Gln Glu Glu Ala Phe Asp Thr Trp Tyr Gly		
171	500	505	510
173	Gly Lys Lys Pro Tyr Asp Tyr Gly Arg Phe Phe Glu Lys Asp Ala Thr		
174	515	520	525
176	His Pro Glu Ala Arg Lys Gly Glu Lys Trp Ser Asp Phe Asp Leu Arg		
177	530	535	540
179	Thr Met Val Glu Arg Gly Lys Asn Asn Pro Ala Ile Phe Met Trp Ser		
180	545	550	555
182	Ile Gly Asn Glu Ile Gly Glu Ala Asn Gly Asp Ala His Ser Leu Ala		
183	565	570	575
185	Thr Val Lys Arg Leu Val Lys Val Ile Lys Asp Val Asp Lys Thr Arg		
186	580	585	590
188	Tyr Val Thr Met Gly Ala Asp Lys Phe Arg Phe Gly Asn Gly Ser Gly		
189	595	600	605
191	Gly His Glu Lys Ile Ala Asp Glu Leu Asp Ala Val Gly Phe Asn Tyr		
192	610	615	620
194	Ser Glu Asp Asn Tyr Lys Ala Leu Arg Ala Lys His Pro Lys Trp Leu		
195	625	630	635
197	Ile Tyr Gly Ser Glu Thr Ser Ser Ala Thr Arg Thr Arg Gly Ser Tyr		
198	645	650	655
200	Tyr Arg Pro Glu Arg Glu Leu Lys His Ser Asn Gly Pro Glu Arg Asn		
201	660	665	670
203	Tyr Glu Gln Ser Asp Tyr Gly Asn Asp Arg Val Gly Trp Gly Lys Thr		
204	675	680	685
206	Ala Thr Ala Ser Trp Thr Phe Asp Arg Asp Asn Ala Gly Tyr Ala Gly		
207	690	695	700
209	Gln Phe Ile Trp Thr Gly Thr Asp Tyr Ile Gly Glu Pro Thr Pro Trp		
210	705	710	715
212	His Asn Gln Asn Gln Thr Pro Val Lys Ser Ser Tyr Phe Gly Ile Val		
213	725	730	735

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215 Asp Thr Ala Gly Ile Pro Lys His Asp Phe Tyr Leu Tyr Gln Ser Gln
216          740          745          750
218 Trp Val Ser Val Lys Lys Lys Pro Met Val His Leu Leu Pro His Trp
219          755          760          765
221 Asn Trp Glu Asn Lys Glu Leu Ala Ser Lys Val Ala Asp Ser Glu Gly
222          770          775          780
224 Lys Ile Pro Val Arg Ala Tyr Ser Asn Ala Ser Ser Val Glu Leu Phe
225 785          790          795          800
227 Leu Asn Gly Lys Ser Leu Gly Leu Lys Thr Phe Asn Lys Lys Gln Thr
228          805          810          815
230 Ser Asp Gly Arg Thr Tyr Gln Glu Gly Ala Asn Ala Asn Glu Leu Tyr
231          820          825          830
233 Leu Glu Trp Lys Val Ala Tyr Gln Pro Gly Thr Leu Glu Ala Ile Ala
234          835          840          845
236 Arg Asp Glu Ser Gly Lys Glu Ile Ala Arg Asp Lys Ile Thr Thr Ala
237          850          855          860
239 Gly Lys Pro Ala Ala Val Arg Leu Ile Lys Glu Asp His Ala Ile Ala
240 865          870          875          880
242 Ala Asp Gly Lys Asp Leu Thr Tyr Ile Tyr Tyr Glu Ile Val Asp Ser
243          885          890          895
245 Gln Gly Asn Val Val Pro Thr Ala Asn Asn Leu Val Arg Phe Gln Leu
246          900          905          910
248 His Gly Gln Gly Gln Leu Val Gly Val Asp Asn Gly Glu Gln Ala Ser
249          915          920          925
251 Arg Glu Arg Tyr Lys Ala Gln Ala Asp Gly Ser Trp Ile Arg Lys Ala
252          930          935          940
254 Phe Asn Gly Lys Gly Val Ala Ile Val Lys Ser Thr Glu Gln Ala Gly
255 945          950          955          960
257 Lys Phe Thr Leu Thr Ala His Ser Asp Leu Leu Lys Ser Asn Gln Val
258          965          970          975
260 Thr Val Phe Thr Gly Lys Lys Glu Gly Gln Glu Lys Thr Val Leu Gly
261          980          985          990
263 Thr Glu Val Pro Lys Val Gln Thr Ile Ile Gly Glu Ala Pro Glu Met
264          995          1000          1005
266 Pro Thr Thr Val Pro Phe Val Tyr Ser Asp Gly Ser Arg Ala Glu Arg
267 1010          1015          1020
269 Pro Val Thr Trp Ser Ser Val Asp Val Ser Lys Pro Gly Ile Val Thr
270 1025          1030          1035          1040
272 Val Lys Gly Met Ala Asp Gly Arg Glu Val Glu Ala Arg Val Glu Val
273          1045          1050          1055
275 Ile Ala Leu Lys Ser Glu Leu Pro Val Val Lys Arg Ile Ala Pro Asn
276          1060          1065          1070
278 Thr Asp Leu Asn Ser Val Asp Lys Ser Val Ser Tyr Val Leu Ile Asp
279          1075          1080          1085
281 Gly Ser Val Glu Glu Tyr Glu Val Asp Lys Trp Glu Ile Ala Glu Glu
282          1090          1095          1100
284 Asp Lys Ala Lys Leu Ala Ile Pro Gly Ser Arg Ile Gln Ala Thr Gly
285 1105          1110          1115          1120
287 Tyr Leu Glu Gly Gln Pro Ile His Ala Thr Leu Val Val Glu Glu Gly

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288          1125          1130          1135
290 Asn Pro Ala Ala Pro Ala Val Pro Thr Val Thr Val Gly Gly Glu Ala
291          1140          1145          1150
293 Val Thr Gly Leu Thr Ser Gln Lys Pro Met Gln Tyr Arg Thr Leu Ala
294          1155          1160          1165
296 Tyr Gly Ala Lys Leu Pro Glu Val Thr Ala Ser Ala Lys Asn Ala Ala
297          1170          1175          1180
299 Val Thr Val Leu Gln Ala Ser Ala Ala Asn Gly Met Arg Ala Ser Ile
300 1185          1190          1195          1200
302 Phe Ile Gln Pro Lys Asp Gly Gly Pro Leu Gln Thr Tyr Ala Ile Gln
303          1205          1210          1215
305 Phe Leu Glu Glu Ala Pro Lys Ile Ala His Leu Ser Leu Gln Val Glu
306          1220          1225          1230
308 Lys Ala Asp Ser Leu Lys Glu Asp Gln Thr Val Lys Leu Ser Val Arg
309          1235          1240          1245
311 Ala His Tyr Gln Asp Gly Thr Gln Ala Val Leu Pro Ala Asp Lys Val
312          1250          1255          1260
314 Thr Phe Ser Thr Ser Gly Glu Gly Glu Val Ala Ile Arg Lys Gly Met
315 1265          1270          1275          1280
317 Leu Glu Leu His Lys Pro Gly Ala Val Thr Leu Asn Ala Glu Tyr Glu
318          1285          1290          1295
320 Gly Ala Lys Asp Gln Val Glu Leu Thr Ile Gln Ala Asn Thr Glu Lys
321          1300          1305          1310
323 Lys Ile Ala Gln Ser Ile Arg Pro Val Asn Val Val Thr Asp Leu His
324          1315          1320          1325
326 Gln Glu Pro Ser Leu Pro Ala Thr Val Thr Val Glu Tyr Asp Lys Gly
327          1330          1335          1340
329 Phe Pro Lys Thr His Lys Val Thr Trp Gln Ala Ile Pro Lys Glu Lys
330 1345          1350          1355          1360
332 Leu Asp Ser Tyr Gln Thr Phe Glu Val Leu Gly Lys Val Glu Gly Ile
333          1365          1370          1375
335 Asp Leu Glu Ala Arg Ala Lys Val Ser Val Glu Gly Ile Val Ser Val
336          1380          1385          1390
338 Glu Glu Val Ser Val Thr Thr Pro Ile Ala Glu Ala Pro Gln Leu Pro
339          1395          1400          1405
341 Glu Ser Val Arg Thr Tyr Asp Ser Asn Gly His Val Ser Ser Ala Lys
342          1410          1415          1420
344 Val Ala Trp Asp Ala Ile Arg Pro Glu Gln Tyr Ala Lys Glu Gly Val
345 1425          1430          1435          1440
347 Phe Thr Val Asn Gly Arg Leu Glu Gly Thr Gln Leu Thr Thr Lys Leu
348          1445          1450          1455
350 His Val Arg Val Ser Ala Gln Thr Glu Gln Gly Ala Asn Ile Ser Asp
351          1460          1465          1470
353 Gln Trp Thr Gly Ser Glu Leu Pro Leu Ala Phe Ala Ser Asp Ser Asn
354          1475          1480          1485
356 Pro Ser Asp Pro Val Ser Asn Val Asn Asp Lys Leu Ile Ser Tyr Asn
357          1490          1495          1500
359 Asn Gln Pro Ala Asn Arg Trp Thr Asn Trp Asn Arg Thr Asn Pro Glu
360 1505          1510          1515          1520

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

PSI

VERIFICATION SUMMARY

DATE: 03/28/2002

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:19634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:364